Prediction of PIK3CA mutation with gene expression

Jun Kang *

* Corresponding author: jkang.alien@gmail.com

Abstract

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Introduction

A list

- Brevity
- Logic and clarity
- Clean typing

The problem

- PIK3CA mutation in selecting drug

Breast cancer with PIK3CA mutation has been approved to use PIK3CA inhibitor in hormone receptor positive HER2 negative subtype. [1] Prediction of PIK3CA mutation was done by gene expression data of TCGA.

- Predicting mutation by gene expression data
    - What for?
    - Feasible?
    - Cost?
- Varing frquency of PIK3CA mutation across cancer types
    - High in endometrial breast
    - not common other cancer type

Universal prediction using gene expression data across cancer type for certain kind of mutation. It's clinically useless now, but we want to explore the possibilities of the PIK3CA mutation prediction.

RNAseq can be widely used. The mutation status directly predictio

Previous study [2]

The proposed solution

Materials and Methods

Dataset

PIK3CA mutation data was get using cgdsr rpackage. Gene expression data was get from GDAC firehose using RTCGAToolbox R package. ER immunostain postive HER2 immunostain negative and/or SISH negative breast cancers are included. Data of invasive ductal carcinomas were used for training set and data of invasive lobular carcinoma were used for test set. Number of observations were 530 in training set and 188 in test set.

Results

Discussion

Main message answers the question and main supporting evidence

Critical assessment opinions on - any shortcomings in study design
- limitations in methods - flaws in analysis - validity of assumption
Comparison with other studies where inconsistencies are discussed
Conclusions comments on possible biological or clinical implications and suggestions for further research.
Evaluate the results - not the authors

References

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